

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/573,939  
Source: JFLWP  
Date Processed by STIC: 04/07/2006

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

**ERROR DETECTED**
**SUGGESTED CORRECTION**
**SERIAL NUMBER:** 10/573,939

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2  Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3  Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4  Non-ASCII      The submitted file was **not saved** in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6  PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7  Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8  Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9  Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10  Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11  Use of <220>  
  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12  PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13  Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/573,939

DATE: 04/07/2006  
TIME: 14:59:41

Input Set : A:\82529.sequence.txt  
Output Set: N:\CRF4\04072006\J573939.raw

W--> 2 Sequenzprotokoll → Pls delete

4 <110> APPLICANT: Epigenomics AG  
6 <120> TITLE OF INVENTION: Verfahren zur Methylierungsanalyse von DNA

C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/573,939

C--> 8 <141> CURRENT FILING DATE: 2006-03-30

W--> 0 <130> FILE REFERENCE:

8 <160> NUMBER OF SEQ ID NOS: 5  
10 <210> SEQ ID NO: 1  
11 <211> LENGTH: 20  
12 <212> TYPE: DNA  
13 <213> ORGANISM: Artificial Sequence

15 <220> FEATURE:

16 <223> OTHER INFORMATION: primer1

18 <400> SEQUENCE: 1

20 gggattattt ttataaggtt

22 <210> SEQ ID NO: 2

23 <211> LENGTH: 23

24 <212> TYPE: DNA

25 <213> ORGANISM: Artificial Sequence

27 <220> FEATURE:

28 <223> OTHER INFORMATION: primer2

30 <400> SEQUENCE: 2

32 tactaaaaac tctaaacccc atc

23

34 <210> SEQ ID NO: 3

35 <211> LENGTH: 21

36 <212> TYPE: DNA

37 <213> ORGANISM: Artificial Sequence

39 <220> FEATURE:

40 <223> OTHER INFORMATION: detection probe1

42 <400> SEQUENCE: 3

21

44 ttcgtcgtagtttcgt t

46 <210> SEQ ID NO: 4

47 <211> LENGTH: 18

48 <212> TYPE: DNA

49 <213> ORGANISM: Artificial Sequence

51 <220> FEATURE:

52 <223> OTHER INFORMATION: detection probe2

54 <400> SEQUENCE: 4

18

56 tagtgagtagc gcgcgggtt

58 <210> SEQ ID NO: 5

59 <211> LENGTH: 25

60 <212> TYPE: DNA

61 <213> ORGANISM: Artificial Sequence

Pls do not use foreign  
Characteris in US application

Does Not Comply  
Corrected Diskette Needed 20

(Pf-1)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/573,939

DATE: 04/07/2006  
TIME: 14:59:41

Input Set : A:\82529.sequence.txt  
Output Set: N:\CRF4\04072006\J573939.raw

63 <220> FEATURE:  
64 <223> OTHER INFORMATION blocker  
66 <400> SEQUENCE: 5  
68 cccatccccca aaaacacaaaa ccaca

25

Invalid Response.  
What is the Source of  
Genetic Material?  
P/s See Item # 11 on  
Error Summary Sheet.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/573,939

DATE: 04/07/2006

TIME: 14:59:42

Input Set : A:\82529.sequence.txt

Output Set: N:\CRF4\04072006\J573939.raw

L:2 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:

L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, &lt;130&gt; FILE REFERENCE